

RAW SEQUENCE LISTING

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Application Serial Number: 10/729,475

Source: IFW

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RAW SEQUENCE LISTING

DATE: 01/26/2005

PATENT APPLICATION: US/10/729,475

TIME: 16:28:32

Input Set : A:\11347612.app

Output Set: N:\CRF4\01262005\J729475.raw

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3 <110> APPLICANT: PAKOLA, STEVE
4   DE SMET, MARK
6 <120> TITLE OF INVENTION: PHARMACOLOGICAL VITREOLYSIS
8 <130> FILE REFERENCE: 113476.122
10 <140> CURRENT APPLICATION NUMBER: 10/729,475
11 <141> CURRENT FILING DATE: 2003-12-05
13 <150> PRIOR APPLICATION NUMBER: GB 0228409.9
14 <151> PRIOR FILING DATE: 2002-12-06
16 <160> NUMBER OF SEQ ID NOS: 15
18 <170> SOFTWARE: PatentIn Ver. 3.2
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 38
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
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26 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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49 <213> ORGANISM: Homo sapiens
51 <220> FEATURE:
52 <221> NAME/KEY: CDS
53 <222> LOCATION: (1)..(747)
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57 Ala Pro Ser Phe Asp Cys Gly Lys Pro Gln Val Glu Pro Lys Lys Cys
58 1 5 10 15
60 cct gga agg gtt gtg ggg ggg tgt gtg gcc cac cca cat tcc tgg ccc
61 Pro Gly Arg Val Gly Gly Cys Val Ala His Pro His Ser Trp Pro
62 20 25 30
64 tgg caa gtc agt ctt aga aca agg ttt gga atg cac ttc tgt gga ggc

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65 Trp Gln Val Ser Leu Arg Thr Arg Phe Gly Met His Phe Cys Gly Gly
66          35          40          45
68 acc ttg ata tcc cca gag tgg gtg ttg act gct gcc cac tgc ttg gag 192
69 Thr Leu Ile Ser Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu Glu
70          50          55          60
72 aag tcc cca agg cct tca tcc tac aag gtc atc ctg ggt gca cac caa 240
73 Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln
74 65          70          75          80
76 gaa gtg aat ctc gaa ccg cat gtt cag gaa ata gaa gtg tct agg ctg 288
77 Glu Val Asn Leu Glu Pro His Val Gln Glu Ile Glu Val Ser Arg Leu
78          85          90          95
80 ttc ttg gag ccc aca cga aaa gat att gcc ttg cta aag cta agc agt 336
81 Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser Ser
82          100          105          110
84 cct gcc gtc atc act gac aaa gta atc cca gct tgt ctg cca tcc cca 384
85 Pro Ala Val Ile Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser Pro
86          115          120          125
88 aat tat gtg gtc gct gac cgg acc gaa tgt ttc atc act ggc tgg gga 432
89 Asn Tyr Val Val Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp Gly
90          130          135          140
92 gaa acc caa ggt act ttt gga gct ggc ctt ctc aag gaa gcc cag ctc 480
93 Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln Leu
94 145          150          155          160
96 cct gtg att gag aat aaa gtg tgc aat cgc tat gag ttt ctg aat gga 528
97 Pro Val Ile Glu Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn Gly
98          165          170          175
100 aga gtc caa tcc acc gaa ctc tgt gct ggg cat ttg gcc gga ggc act 576
101 Arg Val Gln Ser Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr
102          180          185          190
104 gac agt tgc cag ggt gac agt gga ggt cct ctg gtt tgc ttc gag aag 624
105 Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys
106          195          200          205
108 gac aaa tac att tta caa gga gtc act tct tgg ggt ctt ggc tgt gca 672
109 Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala
110          210          215          220
112 cgc ccc aat aag cct ggt gtc tat gtt cgt gtt tca agg ttt gtt act 720
113 Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr
114 225          230          235          240
116 tgg att gag gga gtg atg aga aat aat taa 750
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118          245
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122 <211> LENGTH: 249
123 <212> TYPE: PRT
124 <213> ORGANISM: Homo sapiens
126 <400> SEQUENCE: 4
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128 1          5          10          15
130 Pro Gly Arg Val Val Gly Gly Cys Val Ala His Pro His Ser Trp Pro

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131          20          25          30
133 Trp Gln Val Ser Leu Arg Thr Arg Phe Gly Met His Phe Cys Gly Gly
134          35          40          45
136 Thr Leu Ile Ser Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu Glu
137          50          55          60
139 Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln
140 65          70          75          80
142 Glu Val Asn Leu Glu Pro His Val Gln Glu Ile Glu Val Ser Arg Leu
143          85          90          95
145 Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser Ser
146          100          105          110
148 Pro Ala Val Ile Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser Pro
149          115          120          125
151 Asn Tyr Val Val Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp Gly
152          130          135          140
154 Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln Leu
155 145          150          155          160
157 Pro Val Ile Glu Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn Gly
158          165          170          175
160 Arg Val Gln Ser Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr
161          180          185          190
163 Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys
164          195          200          205
166 Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala
167          210          215          220
169 Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr
170 225          230          235          240
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173          245
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178 <211> LENGTH: 47
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
184 Primer
186 <400> SEQUENCE: 5
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190 <210> SEQ ID NO: 6
191 <211> LENGTH: 27
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
196 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
197 Primer
199 <400> SEQUENCE: 6
200 gcagtgggct gcagtcaaca cccactc 27
203 <210> SEQ ID NO: 7
204 <211> LENGTH: 1047

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205 <212> TYPE: DNA
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210 <222> LOCATION: (1)..(1044)
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215 1 5 10 15
217 gaa gac tgt atg ttt ggg aat ggg aaa gga tac cga ggc aag agg gcg 96
218 Glu Asp Cys Met Phe Gly Asn Gly Lys Gly Tyr Arg Gly Lys Arg Ala
219 20 25 30
221 acc act gtt act ggg acg cca tgc cag gac tgg gct gcc cag gag ccc 144
222 Thr Thr Val Thr Gly Thr Pro Cys Gln Asp Trp Ala Ala Gln Glu Pro
223 35 40 45
225 cat aga cac agc att ttc act cca gag aca aat cca cgg gcg ggt ctg 192
226 His Arg His Ser Ile Phe Thr Pro Glu Thr Asn Pro Arg Ala Gly Leu
227 50 55 60
229 gaa aaa aat tac tgc cgt aac cct gat ggt gat gta ggt ggt ccc tgg 240
230 Glu Lys Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Gly Gly Pro Trp
231 65 70 75 80
233 tgc tac acg aca aat cca aga aaa ctt tac gac tac tgt gat gtc cct 288
234 Cys Tyr Thr Thr Asn Pro Arg Lys Leu Tyr Asp Tyr Cys Asp Val Pro
235 85 90 95
237 cag tgt gcg gcc cct tca ttt gat tgt ggg aag cct caa gtg gag ccg 336
238 Gln Cys Ala Ala Pro Ser Phe Asp Cys Gly Lys Pro Gln Val Glu Pro
239 100 105 110
241 aag aaa tgt cct gga agg gtt gtg ggg ggg tgt gtg gcc cac cca cat 384
242 Lys Lys Cys Pro Gly Arg Val Val Gly Gly Cys Val Ala His Pro His
243 115 120 125
245 tcc tgg ccc tgg caa gtc agt ctt aga aca agg ttt gga atg cac ttc 432
246 Ser Trp Pro Trp Gln Val Ser Leu Arg Thr Arg Phe Gly Met His Phe
247 130 135 140
249 tgt gga ggc acc ttg ata tcc cca gag tgg gtg ttg act gct gcc cac 480
250 Cys Gly Gly Thr Leu Ile Ser Pro Glu Trp Val Leu Thr Ala Ala His
251 145 150 155 160
253 tgc ttg gag aag tcc cca agg cct tca tcc tac aag gtc atc ctg ggt 528
254 Cys Leu Glu Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val Ile Leu Gly
255 165 170 175
257 gca cac caa gaa gtg aat ctc gaa ccg cat gtt cag gaa ata gaa gtg 576
258 Ala His Gln Glu Val Asn Leu Glu Pro His Val Gln Glu Ile Glu Val
259 180 185 190
261 tct agg ctg ttc ttg gag ccc aca cga aaa gat att gcc ttg cta aag 624
262 Ser Arg Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala Leu Leu Lys
263 195 200 205
265 cta agc agt cct gcc gtc atc act gac aaa gta atc cca gct tgt ctg 672
266 Leu Ser Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro Ala Cys Leu
267 210 215 220
269 cca tcc cca aat tat gtg gtc gct gac cgg acc gaa tgt ttc atc act 720

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270 Pro Ser Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys Phe Ile Thr
271 225                230                235                240
273 ggc tgg gga gaa acc caa ggt act ttt gga gct ggc ctt ctc aag gaa 768
274 Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu Leu Lys Glu
275                245                250                255
277 gcc cag ctc cct gtg att gag aat aaa gtg tgc aat cgc tat gag ttt 816
278 Ala Gln Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg Tyr Glu Phe
279                260                265                270
281 ctg aat gga aga gtc caa tcc acc gaa ctc tgt gct ggg cat ttg gcc 864
282 Leu Asn Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly His Leu Ala
283                275                280                285
285 gga ggc act gac agt tgc cag ggt gac agt gga ggt cct ctg gtt tgc 912
286 Gly Gly Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
287 290                295                300
289 ttc gag aag gac aaa tac att tta caa gga gtc act tct tgg ggt ctt 960
290 Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu
291 305                310                315                320
293 ggc tgt gca cgc ccc aat aag cct ggt gtc tat gtt cgt gtt tca agg 1008
294 Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Arg
295                325                330                335
297 ttt gtt act tgg att gag gga gtg atg aga aat aat taa 1047
298 Phe Val Thr Trp Ile Glu Gly Val Met Arg Asn Asn
299                340                345
302 <210> SEQ ID NO: 8
303 <211> LENGTH: 348
304 <212> TYPE: PRT
305 <213> ORGANISM: Homo sapiens
307 <400> SEQUENCE: 8
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311 Glu Asp Cys Met Phe Gly Asn Gly Lys Gly Tyr Arg Gly Lys Arg Ala
312                20                25                30
314 Thr Thr Val Thr Gly Thr Pro Cys Gln Asp Trp Ala Ala Gln Glu Pro
315                35                40                45
317 His Arg His Ser Ile Phe Thr Pro Glu Thr Asn Pro Arg Ala Gly Leu
318 50                55                60
320 Glu Lys Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Gly Gly Pro Trp
321 65                70                75                80
323 Cys Tyr Thr Thr Asn Pro Arg Lys Leu Tyr Asp Tyr Cys Asp Val Pro
324                85                90                95
326 Gln Cys Ala Ala Pro Ser Phe Asp Cys Gly Lys Pro Gln Val Glu Pro
327                100                105                110
329 Lys Lys Cys Pro Gly Arg Val Val Gly Gly Cys Val Ala His Pro His
330                115                120                125
332 Ser Trp Pro Trp Gln Val Ser Leu Arg Thr Arg Phe Gly Met His Phe
333 130                135                140
335 Cys Gly Gly Thr Leu Ile Ser Pro Glu Trp Val Leu Thr Ala Ala His
336 145                150                155                160
338 Cys Leu Glu Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val Ile Leu Gly

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VERIFICATION SUMMARY

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